

GenCore - version 5.1.3
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OM protein - protein search, using sw model

Run on: December 13, 2002, 22:03:23 ; Search time 82 Seconds
(without alignments)
13.690 Million cell updates/sec

Title: US-09-659-737a-2

Perfect score: 293
Sequence: 1 HRDIKAGNILLERIEHDDI.....EWHRITKMSSTAGTYAWMAPE 54

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTRIMBL_21,*
1: sp_archaea:/*
2: sp_bacteria:/*
3: sp_fungi:/*
4: sp_human:/*
5: sp_invertebrate:/*
6: sp_mammal:/*
7: sp_mhc:/*
8: sp_organelle:/*
9: sp_phage:/*
10: sp_plant:/*
11: sp Rodent:/*
12: sp_virus:/*
13: sp_vertebrate:/*
14: sp_unclassified:/*
15: sp_virus:/*
16: sp_bacteria:/*
17: sp_archeap:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

#	Query	Score	Match	Length	DB	ID	Description
1	282	96.2	564	4	09H1Y7	09H1Y7	PRELIMINARY; PRT; 564 AA.
2	278	94.9	570	4	08WWN2	09H1Y7; homo sapien	AC: 09H1Y7; PRELIMINARY; PRT; 564 AA.
3	278	94.9	1036	4	08WWN1	08wwn2 homo sapien	AC: 09H1Y7; PRELIMINARY; PRT; 564 AA.
4	274	93.5	1001	11	08VGD6	08wwn1 homo sapien	AC: 09H1Y7; PRELIMINARY; PRT; 564 AA.
5	239	81.6	69	11	Q9VQ5	08vgd6 mus musculus	AC: 09H1Y7; PRELIMINARY; PRT; 564 AA.
6	239	81.6	1066	4	09H2N5	Q9vq5 mus musculus	AC: 09H1Y7; PRELIMINARY; PRT; 564 AA.
7	231	78.8	847	4	016584	09h2n5 homo sapien	AC: 09H1Y7; PRELIMINARY; PRT; 564 AA.
8	230	78.5	850	11	Q9J1J5	016584 homo sapien	AC: 09H1Y7; PRELIMINARY; PRT; 564 AA.
9	216	73.7	69	11	Q9QVQ4	09j1j5 mus musculus	AC: 09H1Y7; PRELIMINARY; PRT; 564 AA.
10	184	62.8	1020	5	Q9W313	09qvq4 mus musculus	AC: 09H1Y7; PRELIMINARY; PRT; 564 AA.
11	184	62.8	1148	5	Q9VVF6	09w313 drosophila	AC: 09H1Y7; PRELIMINARY; PRT; 564 AA.
12	184	62.8	1161	5	Q95UN8	09vvf6 drosophila	AC: 09H1Y7; PRELIMINARY; PRT; 564 AA.
13	139.5	47.6	977	5	Q9W24	095un8 drosophila	AC: 09H1Y7; PRELIMINARY; PRT; 564 AA.
14	127	43.3	356	10	Q9LZW1	09w24 drosophila	AC: 09H1Y7; PRELIMINARY; PRT; 564 AA.
15	124.5	42.5	859	4	Q9WY25	09lw1 arabidopsis	AC: 09H1Y7; PRELIMINARY; PRT; 564 AA.
16	41.6	346	10	Q9FGS7	Q9wy25 arabidopsis	AC: 09H1Y7; PRELIMINARY; PRT; 564 AA.	

17 121.5 41.5 111 4 Q15450 Q94540 homo sapien
18 121.5 41.5 966 4 Q43283 homo sapien
19 121 41.3 356 10 Q39299 arabidopsis
20 121 41.3 356 10 Q9LM56 arabidopsis
21 121 41.3 978 5 Q8T7Z1 caenorhabdi
22 121 41.3 1040 5 Q8T7Z0 caenorhabdi
23 117 39.9 957 10 Q9FP24 hordeum vulgare
24 114.5 39.1 545 10 Q9S247 Q9S2M7 arabidopsis
25 114 38.9 454 11 Q9ES13 mus musculus
26 114 38.9 455 4 Q9HCC4 Q9HCC5
27 114 38.9 800 4 Q9HDD2 Q9HCC5
28 114 38.9 800 4 Q9NL2 Q9NL2 homo sapien
29 114 38.9 800 4 Q9NEY9 Q9NEY9 homo sapien
30 114 38.9 802 11 Q9ES14 Q9es14 mus musculus
31 114 38.7 405 10 Q9LVQ9 Q9LVQ9 homo sapien
32 113.5 38.7 353 10 Q9FM43 Q9fm43 arabidopsis
33 113 38.6 371 13 Q9QFM3 Q9QFM3 homo sapien
34 113 38.6 663 10 Q8RYH9 Q8ryh9 oryza sativa
35 112.5 38.4 663 10 Q23719 Q23719 arabidopsis
36 111 37.9 406 10 Q8S9K4 Q8s9k4 arabidopsis
37 111 37.9 880 10 Q9L1B8 Q9l1b8 arabidopsis
38 111 37.9 886 10 Q9C9U5 Q9c9u5 arabidopsis
39 111 37.9 1030 10 Q9C9U6 Q9c9u6 arabidopsis
40 110.5 37.7 1151 10 Q9C902 Q9c902 arabidopsis
41 110 37.5 773 10 Q9ARG9 Q9arg9 rosa hybrida
42 109 37.2 227 10 Q9C547 Q9c547 arabidopsis
43 108 36.9 671 10 Q9C547 Q9c547 arabidopsis
44 107.5 36.7 411 10 Q9Q31 Q9q31 arabidopsis
45 107.5 36.7 1338 3 Q60030 Q60030 kluveromyces
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237 107.5 36.7 1338 3 Q60030 Q60030 kluveromyces
238 107.5 36.7 1338 3 Q60030 Q6003

FT	NON_TER	564	564	Query Match	96.2%	Score 282; DB 4; Length 564;
SQ	SEQUENCE	564 AA;	62400 MW;	D4F91E14842E7EEB	CRC64;	
QY	1	HRDIGAGNILLKEIHDIDCNKTLKTDFFGLAREWHRTRKMSLAGTYAWAPE	54	Best Local Similarity	94.4%	Pred. No. 1.5e-28; 2; Mismatches 51; Conservative; 1; Indels 0; Gaps 0;
Db	261	HRDLKSSNILLEKIEHDIDCNKTLKTDFFGLAREWHRTRKMSLAGTYAWAPE	314	Matches 51; Conservative; 2; Mismatches 1; Indels 0; Gaps 0;		
RESULT	2					
Q8WNW2		PRELIMINARY;	PRT;	570 AA.		
ID	Q8WNW2					
AC	Q8WNW2;					
DT	01-MAR-2002	(TREMBrel. 20, Created)				
DT	01-MAR-2002	(TREMBrel. 20, Last sequence update)				
DT	01-JUN-2002	(TREMBrel. 21, Last annotation update)				
DE	Mixed lineage kinase 4alpha.					
GN	MKALPHA.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cetartiodactyla; Homidae; Homo.					
OX	NCB1_TAXID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=HEART;					
RA	Kvasha S., Protopopov A., Rynditch A., Zabavovsky E., Kashuba V.;					
RT	*MK4, a new member of mixed lineage kinases"; Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.					
RL	EMBL: AJ311798; CAC84640.1; -.					
DR	Prints; PRO00452; SH3DOMAIN.					
DR	Prints; PRO0019; TYRKINASE.					
DR	ProDom; PD000001; Euk_pk kinase; 1.					
DR	ProDom; PD000066; SH3; 1.					
DR	SMART; SM00220; S_TK_C; 1.					
DR	SMART; SM00219; TYRK; 1.					
DR	Prosite; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.					
DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.					
DR	Prosite; PS50018; PROTEIN_KINASE_ST; UNKNOWN_1.					
DR	Prosite; PS50002; SH3; 1.					
KW	Kinase.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=HEART;					
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DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.					
DR	Prosite; PS50018; PROTEIN_KINASE_ST; UNKNOWN_1.					
DR	Prosite; PS50002; SH3; 1.					
KW	Kinase.					
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DR	Prints; PRO00452; SH3DOMAIN.					
DR	Prints; PRO0019; TYRKINASE.					
DR	ProDom; PD000001; Euk_pk kinase; 1.					
DR	ProDom; PD000066; SH3; 1.					
DR	SMART; SM00220; S_TK_C; 1.					
DR	SMART; SM00219; TYRK; 1.					
DR	Prosite; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.					
DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.					
DR	Prosite; PS50018; PROTEIN_KINASE_ST; UNKNOWN_1.					
DR	Prosite; PS50002; SH3; 1.					
KW	Kinase.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=HEART;					
RA	Kvasha S., Protopopov A., Rynditch A., Zabavovsky E., Kashuba V.;					
RT	*MK4, a new member of mixed lineage kinases"; Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.					
RL	EMBL: AJ311798; CAC84640.1; -.					
DR	Prints; PRO00452; SH3DOMAIN.					
DR	Prints; PRO0019; TYRKINASE.					
DR	ProDom; PD000001; Euk_pk kinase; 1.					
DR	ProDom; PD000066; SH3; 1.					
DR	SMART; SM00220; S_TK_C; 1.					
DR	SMART; SM00219; TYRK; 1.					
DR	Prosite; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.					
DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.					
DR	Prosite; PS50018; PROTEIN_KINASE_ST; UNKNOWN_1.					
DR	Prosite; PS50002; SH3; 1.					
KW	Kinase.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=HEART;					
RA	Kvasha S., Protopopov A., Rynditch A., Zabavovsky E., Kashuba V.;					
RT	*MK4, a new member of mixed lineage kinases"; Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.					
RL	EMBL: AJ311798; CAC84640.1; -.					
DR	InterPro; IPR00719; Euk_pk kinase.					
DR	InterPro; IPR002290; Ser_thr_pk kinase.					
DR	InterPro; IPR01452; SH3.					
DR	InterPro; IPR01245; Tyr_pk kinase.					
DR	Pfam; PF00059; pk kinase; 1.					
DR	Pfam; PF00018; SH3; 1.					
DR	Prints; PRO00452; SH3DOMAIN.					
DR	ProDom; PD000001; Euk_pk kinase; 1.					
DR	SMART; SM00220; SH3; 1.					
DR	SMART; SM00219; TYRK; 1.					
DR	Prosite; PS50017; PROTEIN_KINASE_ATP; UNKNOWN_1.					
DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.					
DR	Prosite; PS50018; PROTEIN_KINASE_ST; UNKNOWN_1.					
DR	Prosite; PS50002; SH3; 1.					
KW	Kinase.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=HEART;					
RA	Kvasha S., Protopopov A., Rynditch A., Zabavovsky E., Kashuba V.;					
RT	*MK4, a new member of mixed lineage kinases"; Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.					
RL	EMBL: AJ311798; CAC84640.1; -.					
DR	Prints; PRO00452; SH3DOMAIN.					
DR	Prints; PRO0019; TYRKINASE.					
DR	ProDom; PD000001; Euk_pk kinase; 1.					
DR	ProDom; PD000066; SH3; 1.					
DR	SMART; SM00220; S_TK_C; 1.					
DR	SMART; SM00219; TYRK; 1.					
DR	Prosite; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.					
DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.					
DR	Prosite; PS50018; PROTEIN_KINASE_ST; UNKNOWN_1.					
DR	Prosite; PS50002; SH3; 1.					
KW	Kinase.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=HEART;					
RA	Kvasha S., Protopopov A., Rynditch A., Zabavovsky E., Kashuba V.;					
RT	*MK4, a new member of mixed lineage kinases"; Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.					
RL	EMBL: AJ311798; CAC84640.1; -.					
DR	Prints; PRO00452; SH3DOMAIN.					
DR	Prints; PRO0019; TYRKINASE.					
DR	ProDom; PD000001; Euk_pk kinase; 1.					
DR	ProDom; PD000066; SH3; 1.					
DR	SMART; SM00220; S_TK_C; 1.					
DR	SMART; SM00219; TYRK; 1.					
DR	Prosite; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.					
DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.					
DR	Prosite; PS50018; PROTEIN_KINASE_ST; UNKNOWN_1.					
DR	Prosite; PS50002; SH3; 1.					
KW	Kinase.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=HEART;					
RA	Kvasha S., Protopopov A., Rynditch A., Zabavovsky E., Kashuba V.;					
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DR	Prints; PRO00452; SH3DOMAIN.					
DR	Prints; PRO0019; TYRKINASE.					
DR	ProDom; PD000001; Euk_pk kinase; 1.					
DR	ProDom; PD000066; SH3; 1.					
DR	SMART; SM00220; S_TK_C; 1.					
DR	SMART; SM00219; TYRK; 1.					
DR	Prosite; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.					
DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.					
DR	Prosite; PS50018; PROTEIN_KINASE_ST; UNKNOWN_1.					
DR	Prosite; PS50002; SH3; 1.					
KW	Kinase.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=HEART;					
RA	Kvasha S., Protopopov A., Rynditch A., Zabavovsky E., Kashuba V.;					
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DR	ProDom; PD000001; Euk_pk kinase; 1.					
DR	ProDom; PD000066; SH3; 1.					
DR	SMART; SM00220; S_TK_C; 1.					
DR	SMART; SM00219; TYRK; 1.					
DR	Prosite; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.					
DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.					
DR	Prosite; PS50018; PROTEIN_KINASE_ST; UNKNOWN_1.					
DR	Prosite; PS50002; SH3; 1.					
KW	Kinase.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=HEART;					
RA	Kvasha S., Protopopov A., Rynditch A., Zabavovsky E., Kashuba V.;					
RT	*MK4, a new member of mixed lineage kinases"; Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.					
RL	EMBL: AJ311798; CAC84640.1; -.					
DR	Prints; PRO00452; SH3DOMAIN.					
DR	Prints; PRO0019; TYRKINASE.					
DR	ProDom; PD000001; Euk_pk kinase; 1.					
DR	ProDom; PD000066; SH3; 1.					
DR	SMART; SM00220; S_TK_C; 1.					
DR	SMART; SM00219; TYRK; 1.					
DR	Prosite; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.					
DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.					
DR	Prosite; PS50018; PROTEIN_KINASE_ST; UNKNOWN_1.					
DR	Prosite; PS50002; SH3; 1.					
KW	Kinase.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=HEART;					
RA	Kvasha S., Protopopov A., Rynditch A., Zabavovsky E., Kashuba V.;					
RT	*MK4, a new member of mixed lineage kinases"; Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.					
RL	EMBL: AJ311798; CAC84640.1; -.					
DR	Prints; PRO00452; SH3DOMAIN.					
DR	Prints; PRO0019; TYRKINASE.					
DR	ProDom; PD000001; Euk_pk kinase; 1.					
DR	ProDom; PD000066; SH3; 1.					
DR	SMART; SM00220; S_TK_C; 1.					
DR	SMART; SM00219; TYRK; 1.					
DR	Prosite; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.					
DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.					
DR	Prosite; PS50018; PROTEIN_KINASE_ST; UNKNOWN_1.					
DR	Prosite; PS50002; SH3; 1.					
KW	Kinase.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=HEART;					
RA	Kvasha S., Protopopov A., Rynditch A., Zabavovsky E., Kashuba V.;					
RT	*MK4, a new member of mixed lineage kinases"; Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.					
RL	EMBL: AJ311798; CAC84640.1; -.					
DR	Prints; PRO00452; SH3DOMAIN.					
DR	Prints; PRO0019; TYRKINASE.					
DR	ProDom; PD000001; Euk_pk kinase; 1.					
DR	ProDom; PD000066; SH3; 1.					
DR	SMART; SM00220; S_TK_C; 1.					
DR	SMART; SM00219; TYRK; 1.					
DR	Prosite; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.					
DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.					
DR	Prosite; PS50018; PROTEIN_KINASE_ST; UNKNOWN_1.					
DR	Prosite; PS50002; SH3; 1.					
KW	Kinase.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=HEART;					
RA	Kvasha S., Protopopov A., Rynditch A., Zabavovsky E., Kashuba V.;					
RT	*MK4, a new member of mixed lineage kinases"; Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.					
RL	EMBL: AJ311798; CAC84640.1; -.					
DR	Prints; PRO00452; SH3DOMAIN.					
DR	Prints; PRO0019; TYRKINASE.					
DR	ProDom; PD000001; Euk_pk kinase; 1.					
DR	ProDom; PD000066; SH3; 1.					
DR	SMART; SM00220; S_TK_C; 1.					
DR	SMART; SM00219; TYRK; 1.					
DR	Prosite; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.					
DR	Prosite; PS5					

DR	PROSITE; PS50002; SH3; 1.	DT	01-MAY-2000 (TREMBLrel. 13, Created)
KW	ATP-binding; Kinase; SH3 domain; Serine/threonine-protein kinase;	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
SEQUENCE	Transferase; 847 AA; 92687 MW; AFB61930EA281C15 CRC64;	DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)
QY	1 HRDIKAGNILLKIEHHDDCNKTKITDGLAREWHRTKMSAGTYAWAPE 54	DE	Protein tyrosine-serine/threonine kinase (Fragment).
Db	239 HRDLKSNINLILQPIESDDMHEKTKITDGLAREWHKTOMSAAGTYAWAPE 292	OS	Mus sp.
Query Match	78.8%; Score 231; DB 4; Length 847;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Best Local Similarity	77.8%; Pred. No. 1 2e-21; 7; Mismatches 5; Indels 0; Gaps 0;	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Matches	42; Conservative	OX	NCBI_TAXID=10095;
RESULT	8	RN	[1]
ID	Q9JJ15	RP	SEQUENCE FROM N.A.
AC	Q9JJ15;	RX	MEDLINE=96043742; PubMed=7591219;
DT	01-OCT-2000 (TREMBLrel. 15, Created)	RX	"Protein tyrosine kinase expression during the estrous cycle and carcinogenesis of the mammary gland.";
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	RL	Int. J. Cancer 63:288-295(1995).
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)	DR	IntePro; IPRO0071; Euk_Pkinase.
DE	Mixed lineage kinase 3.	DR	ProDom; PD00001; Euk_Pkinase; 1.
GN	MLK3.	DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
OS	Mus musculus (Mouse)	DR	SEQUENCE FROM N.A.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	DR	MEDLINE=96043742; PubMed=7591219;
OX	NCBI_TAXID=10090;	DR	"Protein tyrosine kinase expression during the estrous cycle and carcinogenesis of the mammary gland.";
RN	[1]	RL	Int. J. Cancer 63:288-295(1995).
RP	SEQUENCE FROM N.A.	DR	IntePro; IPRO0071; Euk_Pkinase.
RC	STRAIN=129-Ola;	DR	ProDom; PD00009; Pkinase; 1.
RX	MEDLINE=20354997; PubMed=10894943;	DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
RA	Saridaki A., Ferraz C., Demaile J., Scherer G., Roux A.-F.;	DR	SEQUENCE FROM N.A.
RT	"Genomic sequencing reveals the structure of the Kcnk6 and Map3k11 genes and their close vicinity to the Sipal gene on mouse chromosome 19."	DR	MEDLINE=96043742; PubMed=7591219;
RT	;	DR	"Protein tyrosine kinase expression during the estrous cycle and carcinogenesis of the mammary gland.";
RL	Cytogenet. Cell Genet. 89:85-88(2000).	RL	Int. J. Cancer 63:288-295(1995).
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.	DR	IntePro; IPRO0071; Euk_Pkinase.
CC	-1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.	DR	ProDom; PD00001; Euk_Pkinase; 1.
DR	EMBL; AF151142; AAF73281.1; -.	DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR	HESSP; P29355; ISEM;	DR	SEQUENCE FROM N.A.
DR	InterPro; IPR000719; Euk_pk kinase.	DR	STRAIN=20354997; PubMed=10894943;
DR	InterPro; IPR001245; Tyr_pk kinase.	DR	RA
DR	InterPro; IPR002290; Ser_thr_pk kinase.	RA	Q9W313
DR	Pfam; PF00065; Pkinase; 1.	RA	PRELIMINARY; PRT; 1020 AA.
DR	PRINTS; PR00452; SH3DOMAIN.	RA	09W313
DR	PRINTS; PR00109; TYRKINASE.	RA	09W313
DR	PRODOM; PD000001; Euk_pk kinase; 1.	RA	09W313
DR	SMART; SM00326; SH3; 1.	RA	09W313
DR	SMART; SM00219; TYRK; 1.	RA	09W313
DR	PROSITE; PS000219; PROTEIN_KINASE_ATP; 1.	RA	09W313
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.	RA	09W313
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.	RA	09W313
DR	PROSITE; PS50002; SH3; 1.	RA	09W313
KW	ATP-binding; Kinase; SH3 domain; serine/threonine-protein kinase; Transferase.	RA	09W313
SEQUENCE	850 AA; 93199 MW; 8F026CB3532DC10E CRC64;	RA	09W313
QY	1 HRDIKAGNILLKIEHHDDCNKTKITDGLAREWHRTKMSAGTYAWAPE 54	RA	09W313
Db	240 HRDLKSNINLILQPIESDDMHEKTKITDGLAREWHKTOMSAAGTYAWAPE 293	RA	09W313
Query Match	78.5%; Score 230; DB 11; Length 850;	RA	09W313
Best Local Similarity	77.8%; Pred. No. 1.6e-21; 7; Mismatches 5; Indels 0; Gaps 0;	RA	09W313
Matches	42; Conservative	RA	09W313
RESULT	9	RA	09W313
Db	09QV04	RA	09QV04
AC	09QV04; PRELIMINARY; PRT; 69 AA.	RA	09QV04

